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OM nucleic - nucleic search, using bw model

Run on: August 28, 2006, 09:45:23 ; Search time 150 seconds
(without alignments)
424.118 Million cell updates/sec

Title: US-09-847-601B-100
Sequence: 1 ucgaacugaugagccgucgcgcgaacgaag 34

Scoring table: OLIGO_NIC
Gapop 60.0, Gapext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2806514

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Issued Patents NM:*

- 1: /EMC Celerra SIDS3/prodata/2/ina/1 COMB.seq:*
- 2: /EMC Celerra SIDS3/prodata/2/ina/5 COMB.seq:*
- 3: /EMC Celerra SIDS3/prodata/2/ina/6 COMB.seq:*
- 4: /EMC Celerra SIDS3/prodata/2/ina/6 COMB.seq:*
- 5: /EMC Celerra SIDS3/prodata/2/ina/7 COMB.seq:*
- 6: /EMC Celerra SIDS3/prodata/2/ina/H COMB.seq:*
- 7: /EMC Celerra SIDS3/prodata/2/ina/H COMB.seq:*
- 8: /EMC Celerra SIDS3/prodata/2/ina/H COMB.seq:*
- 9: /EMC Celerra SIDS3/prodata/2/ina/H COMB.seq:*
- 10: /EMC Celerra SIDS3/prodata/2/ina/backfillseq1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	100.0	34	US-09-874-601-100	Sequence 100, App
2	27	79.4	32	US-09-874-601-101	Sequence 101, App
3	27	79.4	34	US-09-874-601-98	Sequence 98, Appl
4	26	76.5	34	US-09-874-601-92	Sequence 92, Appl
5	26	76.5	34	US-09-874-601-93	Sequence 93, Appl
6	26	76.5	34	US-09-874-601-99	Sequence 99, Appl
7	25	73.5	34	US-09-874-601-90	Sequence 90, Appl
8	25	73.5	34	US-09-874-601-91	Sequence 91, Appl
9	25	73.5	34	US-09-874-601-95	Sequence 95, Appl
10	25	73.5	34	US-09-874-601-96	Sequence 96, Appl
11	25	73.5	34	US-09-874-601-97	Sequence 97, Appl
12	19	55.9	34	US-09-874-601-94	Sequence 94, Appl
13	15	44.1	333	US-09-489-039A-3537	Sequence 3537, Ap
14	15	44.1	601	US-09-949-016-81813	Sequence 81813, A
15	15	44.1	1152	US-09-045-186-1	Sequence 1, Appl
16	15	44.1	1152	US-09-045-186-3	Sequence 3, Appl
17	15	44.1	1338	PCT-US93-05039-2	Sequence 2, Appl
18	15	44.1	1534	PCT-US93-05039-1	Sequence 1, Appl
19	15	44.1	1605	US-09-676-970-1	Sequence 1, Appl
20	15	44.1	1605	US-09-676-972B-1	Sequence 1, Appl
21	15	44.1	1605	US-09-016-434-1231	Sequence 1231, Ap
22	15	44.1	1605	US-09-676-941A-1	Sequence 1, Appl
23	15	44.1	1605	US-10-013-846-3	Sequence 3, Appl

24	15	44.1	1605	US-10-291-446-1	Sequence 1, Appl
25	15	44.1	1605	US-10-410-648-3	Sequence 3, Appl
26	15	44.1	1605	US-10-274-851-3	Sequence 3, Appl
27	15	44.1	1991	US-09-270-767-11487	Sequence 11487, A
28	15	44.1	2634	US-08-232-144-3	Sequence 3, Appl
29	15	44.1	2634	US-09-708-392-10	Sequence 10, Appl
30	15	44.1	4571	US-08-232-144-5	Sequence 5, Appl
31	15	44.1	12001	US-08-458-568A-11	Sequence 11, Appl
32	15	44.1	125192	US-09-949-016-14120	Sequence 14120, A
33	15	44.1	127687	US-09-949-016-121350	Sequence 121350, A
34	15	44.1	4403765	US-09-103-840A-2	Sequence 2, Appl
35	15	44.1	4411529	US-09-103-840A-1	Sequence 1, Appl
36	15	41.2	36	US-08-334-847-806	Sequence 806, Appl
37	14	41.2	38	US-09-371-772B-11589	Sequence 11589, A
38	14	41.2	38	US-09-371-772B-11932	Sequence 11932, A
39	14	41.2	38	US-10-138-674B-11865	Sequence 11865, A
40	14	41.2	38	US-10-138-674B-14209	Sequence 14209, A
41	14	41.2	491	US-09-640-211A-529	Sequence 529, App
42	14	41.2	498	US-09-302-540-8002	Sequence 8002, Ap
43	14	41.2	570	US-09-328-352-2408	Sequence 2408, Ap
44	14	41.2	601	US-09-949-016-121350	Sequence 121350, A
45	14	41.2	601	US-09-533-559-3649	Sequence 3649, Ap

ALIGNMENTS

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RESULT 1
US-09-874-601-100
; Sequence 100, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 100
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..7)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-100
Query Match      100.0%; Score 34; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.1e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy      1 UGCAACTUGAGUGAGCCGUGUGCGCGCAAGCAAG 34
Db      1 UGCAACTUGAGUGAGCCGUGUGCGCGCAAGCAAG 34
RESULT 2
US-09-874-601-101
; Sequence 101, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.

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Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AACUGAGCGCGUCCGGCGGAAC 30
Db 5 AACUGAGCGCGUCCGGCGGAAC 30

RESULT 6
US-09-874-601-99
; Sequence 99, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1997-05-01
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 99
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-99

Query Match 76.5%; Score 26; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 AACUGAGCGCGUCCGGCGGAAC 30
Db 5 AACUGAGCGCGUCCGGCGGAAC 30

RESULT 7
US-09-874-601-90
; Sequence 90, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 90
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-90

Query Match 73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCGCGUCCGGCGGAAC 30
Db 6 ACUGAUGAGCGCGUCCGGCGGAAC 30

RESULT 8
US-09-874-601-91
; Sequence 91, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1997-05-01
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 91
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1..1)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-91

Query Match 73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCGCGUCCGGCGGAAC 30
Db 6 ACUGAUGAGCGCGUCCGGCGGAAC 30

RESULT 9
US-09-874-601-95
; Sequence 95, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: US/09/874,601
; PRIOR FILING DATE: 1997-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 95
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence

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; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..34)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-95

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 10
US-09-874-601-96
; Sequence 96, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874.601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..34)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-96

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 11
US-09-874-601-97
; Sequence 97, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
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; CURRENT APPLICATION NUMBER: US/09/874.601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 97
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..34)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-97

Query Match      73.5%; Score 25; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACUGAUGAGCGGUCGCGCGGAAC 30
DB      6 ACUGAUGAGCGGUCGCGCGGAAC 30

RESULT 12
US-09-874-601-94
; Sequence 94, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHOD
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874.601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 94
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1..34)
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-94

Query Match      55.9%; Score 19; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 GAGCGGUCGCGCGGAAC 30
DB      12 GAGCGGUCGCGCGGAAC 30

RESULT 13
US-09-489-039A-3537/c
; Sequence 3537, Application US/09489039A
; Patent No. 6610836
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; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3537
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3537

Query Match      44.1%; Score 15; DB 3; Length 333;
Best Local Similarity 86.7%; Pred. No. 26;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      15 CCGTCCGCGCGGAAA 29
DB      62 CCGTCCGCGCGGAAA 48

RESULT 14
US-09-949-016-81813
; Sequence 81813, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CA001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81813
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-81813

Query Match      44.1%; Score 15; DB 3; Length 601;
Best Local Similarity 80.0%; Pred. No. 26;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 UGCAACUGAGGAC 15
DB      41 TGCACACTGATGAC 55

RESULT 15
US-09-045-186-1
; Sequence 1, Application US/09045186
; Patent No. 6087154
; GENERAL INFORMATION:
; APPLICANT: Baez, Melvyn
; APPLICANT: Cates, Carolyn A.
; TITLE OF INVENTION: RHESUS NEUROPEPTIDE Y1 RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESS: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
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; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/045,186
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: P-11376
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1152 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1152
US-09-045-186-1

Query Match      44.1%; Score 15; DB 3; Length 1152;
Best Local Similarity 73.3%; Pred. No. 26;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      6 ACTGATGAGCCGTC 20
DB      538 ACTGATGAGCCGTC 552
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Search completed: August 28, 2006, 10:29:28
Job time : 154 secs

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CC polypeptide or peptide selected from the group of rod opsin, *rhodopsin*, *transducin*, *phosphodiesterase*, *phospholipase C*, *phospholipase A2*, *phospholipase A1*, *phospholipase A3*, *phospholipase A4*, *phospholipase A5*, or *phospholipase A6*; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell expressing the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (1) has ophthalmological activity, and can be used in gene therapy. (1) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction, (diabetic) retinopathy, or (age-related) macular degeneration. (1) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (1) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pitted lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. ABZ72763 to ABZ72953 represent sequences used in the exemplification of the present invention

Sequence 34 BP; 10 A; 8 C; 11 G; 0 T; 5 U; 0 Other;

Query Match	100.0%	Score 34	DB 10	Length 34
Best Local Similarity	100.0%	Pred. NC	6.9e-09	
Matches 34	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Dy 1 UGCAAACTGAUGAGCCGUUCCGGCGGCAAA CGAAG 34
|||
Db 1 UGCAAACTGAUGAGCCGUUCCGGCGGCAAA CGAAG 34

RESULT 2
ABZ72866
ID ABZ72866 standard; RNA; 32 BP.

AC ABZ72866;

DT 09-APR-2003 (first entry)

DE IGF1 R22 exemplary ribozyme construct SEQ ID NO:101.

kw Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

diabetic retinopathy; macular degeneration; autosomal dominant retinitis;

XX

OS Synthetic.

PN WO200288320-A2.

PD 07-NOV-2002

PF 01-MAY-2002; 2002WO-US013679.

PR 01-MAY-2001; 2001US-00847601.

PA (UYFL) UNIV FLORIDA.

PI Lewin AS, Shaw LC, Grant MB;

DR WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition, useful for treating a disease or dysfunction of the mammalian eye e.g. retinal disease, e.g. diabetic retinopathy or age-related macular degeneration.

PS Claim 1; Page 81; 115pp; English.

The present invention describes a recombinant adeno-associated virus (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a first ribozyme that specifically cleaves an mRNA encoding a protein, polypeptide, or peptide selected from the group of rod opsin, *INOS*, *RGS/peripherin*, *VEGFR1*, *VEGFR2*, *adenosine A-2B receptor*, *IGF-1*, *integrin alpha 1*, *integrin alpha 3*, *integrin alpha 5*, or *integrin alpha V*; (b) a vector comprising a polynucleotide encoding the ribozyme, where the polynucleotide operably positioned downstream of at least a first promoter that directs expression of the polynucleotide in a selected mammalian cell transformed with the vector; (c) a viral particle comprising the ribozyme or the polynucleotide; (d) an AAV vector comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (I) has ophthalmological activity, and can be used in gene therapy. (I) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal dysfunction, (diabetic) retinopathy, or (age-related) macular degeneration.. (I) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (I) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. AB272763 to AB272951 represent sequences used in the exemplification of the present invention

sq Sequence 32 BP; 8 A; 8 C; 11 G; 0 T; 5 U; 0 Other;

Query Match	79.4%	Score 27	DB 10	Length 32
Best Local Similarity	100.0%	Pred. No.	4.7e-05	
Matches 27	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Oy	5 AACUGAUGCCTGCGGGCAACG 31
D8	3 AACTGAUAGCCGTTCGCGGAACG 29

RESULT 3
ABZ72863
ID ABZ72863 standard; RNA; 34 BP.

AC ABZ72863 ;

DT 09-APR-2003 (first entry)

DE Alpha V R21 exemplary ribozyme construct SEQ ID NO:98.

KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

KW diabetic retinopathy; macular degeneration; autosomal dominant retinitis;

XX

XX

XX

XX

XX

XX

XX Lewin AS, Shaw LC, Grant MB;
PI
XX WPI; 2003-111880/10.
DR

PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

PS Claim 1, Page 80, 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 7 A; 10 C; 13 G; 0 T; 4 U; 0 Other;

Query Match 79.4%; Score 27; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-05;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAGAGCCGUCGCGGGAACG 31
Db 5 AACUGAGAGCCGUCGCGGGAACG 31

RESULT 4
AB272857
ID AB272857 standard; RNA; 34 BP.

XX AB272857;

DT 09-APR-2003 (first entry)

DE Alpha 3 R21 exemplary ribozyme construct SEQ ID NO:92.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

OS Synthetic.

PN WO20028320-A2.

PD 07-NOV-2002.

PF 01-MAY-2002; 2002WO-US013679.

PR 01-MAY-2001; 2001US-00847601.

PA (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;
PI WPI; 2003-111860/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

PS Claim 1, Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 10 A; 8 C; 10 G; 0 T; 6 U; 0 Other;

Query Match 76.5%; Score 26; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AACUGAGAGCCGUCGCGGGAAC 30
Db 5 AACUGAGAGCCGUCGCGGGAAC 30

RESULT 5
AB272858
ID AB272858 standard; RNA; 34 BP.

XX AB272858;

DT 09-APR-2003 (first entry)

DE Alpha 3 R22 exemplary ribozyme construct SEQ ID NO:93.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

OS Synthetic.

PN WO20028320-A2.

PD 07-NOV-2002.

PP 01-MAY-2002; 2002MO-US013679.
 XX
 PR 01-MAY-2001; 2001US-00847601.
 XX
 PA (UYFL) UNIV FLORIDA.
 XX
 PI Lewin AS, Shaw LC, Grant MB;
 XX
 DR WPI; 2003-111880/10.
 XX
 PT A recombinant adeno-associated virus-vectored ribozyme composition,
 PT useful for treating a disease or dysfunction of the mammalian eye e.g.
 PT retinal disease, e.g. diabetic retinopathy or age-related macular
 PT degeneration.
 XX
 PS Claim 1; Page 80; 115pp; English.
 XX
 CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the ribozyme or the polynucleotide. Also described is a method
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC local vision. AB272763 to AB272953 represent sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
 CC
 CC Query Match 76.5%; Score 26; DB 10; Length 34;
 CC Best Local Similarity 100.0%; Pred. No. 0.00016;
 CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 5 AACUGAUGAGCCGUCGCGCGGAAC 30
 CC ||||||||||||||||||||||||||||
 CC 5 AACUGAUGAGCCGUCGCGCGGAAC 30
 CC
 CC RESULT 6
 CC AB272873
 CC ID AB272873 standard; RNA; 34 BP.
 CC
 CC AC AB272873;
 CC
 CC DT 09-APR-2003 (first entry)
 CC
 CC DE VEGFR2 R22 exemplary ribozyme construct SEQ ID NO:114.
 CC
 CC XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
 CC XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
 CC XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
 CC XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
 CC
 CC QS Synthetic.

XX
 PN W020028320-A2.
 XX
 PD 07-NOV-2002.
 XX
 XX 01-MAY-2002; 2002MO-US013679.
 XX
 PR 01-MAY-2001; 2001US-00847601.
 XX
 XX (UYFL) UNIV FLORIDA.
 XX
 PI Lewin AS, Shaw LC, Grant MB;
 XX
 DR WPI; 2003-111880/10.
 XX
 PT A recombinant adeno-associated virus-vectored ribozyme composition,
 PT useful for treating a disease or dysfunction of the mammalian eye e.g.
 PT retinal disease, e.g. diabetic retinopathy or age-related macular
 PT degeneration.
 XX
 PS Claim 1; Page 81; 115pp; English.
 XX
 CC The present invention describes a recombinant adeno-associated virus
 CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
 CC first ribozyme that specifically cleaves an mRNA encoding a protein,
 CC polypeptide, or peptide selected from the group of rod opsin, INOS,
 CC RDS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
 CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
 CC vector comprising a polynucleotide encoding the ribozyme, where the
 CC polynucleotide operably positioned downstream of at least a first
 CC promoter that directs expression of the polynucleotide in a selected
 CC mammalian cell transformed with the vector; (c) a viral particle
 CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
 CC comprising the ribozyme or the polynucleotide; or (e) a host cell
 CC comprising the ribozyme or the polynucleotide. Also described is a method
 CC for decreasing the amount of mRNA encoding a selected polypeptide in a
 CC retinal cell of a mammalian eye, comprising providing to the eye the
 CC composition described above, and for a time effective to specifically
 CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
 CC be used in gene therapy. (I) can be used for treating a disease or
 CC dysfunction of the mammalian eye, such as a retinal disease or retinal
 CC dysfunction, (diabetic) retinopathy, or (age-related) macular
 CC degeneration. (I) is also useful for manufacturing a medicament for
 CC treating the diseases mentioned above, including autosomal dominant
 CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
 CC for treating, decreasing the severity, or ameliorating the symptoms of a
 CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
 CC blindness, a reduction in central or peripheral vision, or a reduction in
 CC local vision. AB272763 to AB272953 represent sequences used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 34 BP; 10 A; 7 C; 9 G; 0 T; 8 U; 0 Other;
 CC
 CC Query Match 76.5%; Score 26; DB 10; Length 34;
 CC Best Local Similarity 100.0%; Pred. No. 0.00016;
 CC Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC 5 AACUGAUGAGCCGUCGCGCGGAAC 30
 CC ||||||||||||||||||||||||||||
 CC 5 AACUGAUGAGCCGUCGCGCGGAAC 30
 CC
 CC RESULT 7
 CC AB272864
 CC ID AB272864 standard; RNA; 34 BP.
 CC
 CC AC AB272864;
 CC
 CC DT 09-APR-2003 (first entry)
 CC
 CC DE Alpha V R22 exemplary ribozyme construct SEQ ID NO:99.
 CC
 CC XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;

XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
OS Synthetic.
XX WO200288320-A2.
XX 07-NOV-2002.
XX 01-MAY-2002; 2002WO-US013679.
XX 01-MAY-2001; 2001US-00847601.
XX (UYFL) UNIV FLORIDA.
XX Lewin AS, Shaw LC, Grant MB;
XX WPI; 2003-111880/10.
XX A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX Claim 1; Page 80; 115pp; English.
XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2b receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (1) has ophthalmological activity, and can
CC be used in gene therapy. (1) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (1) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB2728763 to AB272953 represent sequences used in the
XX exemplification of the present invention
XX Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;
SO Query Match 76.5%; Score 26; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAGAGCCGUCGCGGGAAC 30
DB 5 AACUGAGAGCCGUCGCGGGAAC 30
RESULT 8
AB272872
ID AB272872 standard; RNA; 34 BP.
XX AC AB272872;
XX

DT 09-APR-2003 (first entry)
XX DE VEGFR2 R21 exemplary ribozyme construct SEQ ID NO:113.
XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX OS Synthetic.
XX WO200288320-A2.
XX 07-NOV-2002.
XX 01-MAY-2002; 2002WO-US013679.
XX 01-MAY-2001; 2001US-00847601.
XX (UYFL) UNIV FLORIDA.
XX Lewin AS, Shaw LC, Grant MB;
XX WPI; 2003-111880/10.
XX A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX Claim 1; Page 81; 115pp; English.
XX The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, INOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2b receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (1) has ophthalmological activity, and can
CC be used in gene therapy. (1) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (1) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB2728763 to AB272953 represent sequences used in the
XX exemplification of the present invention
XX Sequence 34 BP; 10 A; 9 C; 10 G; 0 T; 5 U; 0 Other;
SO Query Match 76.5%; Score 26; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 AACUGAGAGCCGUCGCGGGAAC 30
DB 5 AACUGAGAGCCGUCGCGGGAAC 30
RESULT 9

AB272855
ID AB272855 standard; RNA; 34 BP.
XX
AC AB272855;
XX
DT 09-APR-2003 (first entry)
XX
DE A2B R21 exemplary ribozyme construct SEQ ID NO:90.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Claim 1; Page 80; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 34 BP; 10 A; 8 C; 10 G; 0 T; 6 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 ACUGAUGAGCCGUGCGCGGAAC 30

Db
6 ACUGAUGAGCCGUGCGCGGAAC 30
|||||
RESULT 10
AB272862
ID AB272862 standard; RNA; 34 BP.
XX
AC AB272862;
XX
DT 09-APR-2003 (first entry)
XX
DE Alpha 1 R22 exemplary ribozyme construct SEQ ID NO:97.
XX
KW Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KM ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KM blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.
XX
OS Synthetic.
XX
PN WO200288320-A2.
XX
PD 07-NOV-2002.
XX
PF 01-MAY-2002; 2002WO-US013679.
XX
PR 01-MAY-2001; 2001US-00847601.
XX
PA (UYFL) UNIV FLORIDA.
XX
PI Lewin AS, Shaw LC, Grant MB;
XX
DR WPI; 2003-111880/10.
XX
PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.
XX
PS Claim 1; Page 80; 115pp; English.
XX
CC The present invention describes a recombinant adeno-associated virus
CC (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
CC first ribozyme that specifically cleaves an mRNA encoding a protein,
CC polypeptide, or peptide selected from the group of rod opsin, iNOS,
CC RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
CC alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
CC vector comprising a polynucleotide encoding the ribozyme, where the
CC polynucleotide operably positioned downstream of at least a first
CC promoter that directs expression of the polynucleotide in a selected
CC mammalian cell transformed with the vector; (c) a viral particle
CC comprising the ribozyme or the polynucleotide; (d) an AAV vector
CC comprising the ribozyme or the polynucleotide; or (e) a host cell
CC comprising the ribozyme or the polynucleotide. Also described is a method
CC for decreasing the amount of mRNA encoding a selected polypeptide in a
CC retinal cell of a mammalian eye, comprising providing to the eye the
CC composition described above, and for a time effective to specifically
CC cleave the mRNA in the cell. (I) has ophthalmological activity, and can
CC be used in gene therapy. (I) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC degeneration, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (I) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. AB272763 to AB272953 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 34 BP; 7 A; 10 C; 9 G; 0 T; 8 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAGUAGCCGUCGCGGCAAC 30
DB 6 ACTGAGUAGCCGUCGCGGCAAC 30

RESULT 11

ABZ72856
ID ABZ72856 standard; RNA; 34 BP.

AC ABZ72856;

DT 09-APR-2003 (first entry)

DB A2B R22 exemplary ribozyme construct SEQ ID NO:91.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

XX Synthetic.

XX MO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002MO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RNS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide; or (e) a host cell
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration. (I) is also useful for manufacturing a medicament for
XX treating the diseases mentioned above, including autosomal dominant
XX retinitis or a blood-retinal barrier dysfunction. (I) can also be useful
XX for treating, decreasing the severity, or ameliorating the symptoms of a
XX pathological condition, e.g. atrophic or pigmented lesions of the eye,
XX blindness, a reduction in central or peripheral vision, or a reduction in

CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention
XX

SQ Sequence 34 BP; 9 A; 8 C; 11 G; 0 T; 6 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACTGAGUAGCCGUCGCGGCAAC 30
DB 6 ACTGAGUAGCCGUCGCGGCAAC 30

RESULT 12

ABZ72870
ID ABZ72870 standard; RNA; 34 BP.

AC ABZ72870;

DT 09-APR-2003 (first entry)

DB VEGFR1 R21 exemplary ribozyme construct SEQ ID NO:111.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
KW ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
KM diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
KW blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

XX Synthetic.

XX MO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002MO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

PT A recombinant adeno-associated virus-vectored ribozyme composition,
PT useful for treating a disease or dysfunction of the mammalian eye e.g.
PT retinal disease, e.g. diabetic retinopathy or age-related macular
PT degeneration.

XX Claim 1; Page 81; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (I). (I) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, INOS,
XX RNS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide; or (e) a host cell
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically
XX cleave the mRNA in the cell. (I) has ophthalmological activity, and can
XX be used in gene therapy. (I) can be used for treating a disease or
XX dysfunction of the mammalian eye, such as a retinal disease or retinal
XX degeneration. (I) is also useful for manufacturing a medicament for

CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 8 A; 12 C; 8 G; 0 T; 6 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCCGUCGCGCGGAAC 30
Db 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 13
ABZ72860
ID ABZ72860 standard; RNA; 34 BP.

XX ABZ72860;

XX 09-APR-2003 (first entry)

DE Alpha 5 R22 exemplary ribozyme construct SEQ ID NO:95.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

XX Synthetic.

XX WO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, inos,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector
XX comprising the ribozyme or the polynucleotide. Also described is a method
XX for decreasing the amount of mRNA encoding a selected polypeptide in a
XX retinal cell of a mammalian eye, comprising providing to the eye the
XX composition described above, and for a time effective to specifically

CC cleave the mRNA in the cell. (1) has ophthalmological activity, and can
CC be used in gene therapy. (1) can be used for treating a disease or
CC dysfunction of the mammalian eye, such as a retinal disease or retinal
CC dysfunction, (diabetic) retinopathy, or (age-related) macular
CC degeneration. (1) is also useful for manufacturing a medicament for
CC treating the diseases mentioned above, including autosomal dominant
CC retinitis or a blood-retinal barrier dysfunction. (1) can also be useful
CC for treating, decreasing the severity, or ameliorating the symptoms of a
CC pathological condition, e.g. atrophic or pigmented lesions of the eye,
CC blindness, a reduction in central or peripheral vision, or a reduction in
CC total vision. ABZ72763 to ABZ72953 represent sequences used in the
CC exemplification of the present invention

XX Sequence 34 BP; 8 A; 8 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ACUGAUGAGCCGUCGCGCGGAAC 30
Db 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 14
ABZ72861
ID ABZ72861 standard; RNA; 34 BP.

XX ABZ72861;

XX 09-APR-2003 (first entry)

DE Alpha 1 R21 exemplary ribozyme construct SEQ ID NO:96.

XX Hairpin ribozyme; hammerhead ribozyme; ribozyme; retinal disease; target;
XX ophthalmological; gene therapy; eye; retinal dysfunction; AAV;
XX diabetic retinopathy; macular degeneration; autosomal dominant retinitis;
XX blood-retinal barrier dysfunction; adeno-associated virus; blindness; ss.

XX Synthetic.

XX WO200288320-A2.

XX 07-NOV-2002.

XX 01-MAY-2002; 2002WO-US013679.

XX 01-MAY-2001; 2001US-00847601.

XX (UYFL) UNIV FLORIDA.

XX Lewin AS, Shaw LC, Grant MB;

XX WPI; 2003-111880/10.

XX A recombinant adeno-associated virus-vectored ribozyme composition,
XX useful for treating a disease or dysfunction of the mammalian eye e.g.
XX retinal disease, e.g. diabetic retinopathy or age-related macular
XX degeneration.

XX Claim 1; Page 80; 115pp; English.

XX The present invention describes a recombinant adeno-associated virus
XX (AAV) vectored ribozyme composition (1). (1) comprises: (a) at least a
XX first ribozyme that specifically cleaves an mRNA encoding a protein,
XX polypeptide, or peptide selected from the group of rod opsin, inos,
XX RGS/peripherin, VEGFR1, VEGFR2, adenosine A-2B receptor, IGF-1, integrin
XX alpha 1, integrin alpha 3, integrin alpha 5, or integrin alpha V; (b) a
XX vector comprising a polynucleotide encoding the ribozyme, where the
XX polynucleotide operably positioned downstream of at least a first
XX promoter that directs expression of the polynucleotide in a selected
XX mammalian cell transformed with the vector; (c) a viral particle
XX comprising the ribozyme or the polynucleotide; (d) an AAV vector

comprising the ribozyme or the polynucleotide; or (e) a host cell comprising the ribozyme or the polynucleotide. Also described is a method for decreasing the amount of mRNA encoding a selected polypeptide in a retinal cell of a mammalian eye, comprising providing to the eye the composition described above, and for a time effective to specifically cleave the mRNA in the cell. (1) has ophthalmological activity, and can be used in gene therapy. (1) can be used for treating a disease or dysfunction of the mammalian eye, such as a retinal disease or retinal degeneration. (1) is also useful for manufacturing a medicament for treating the diseases mentioned above, including autosomal dominant retinitis or a blood-retinal barrier dysfunction. (1) can also be useful for treating, decreasing the severity, or ameliorating the symptoms of a pathological condition, e.g. atrophic or pigmented lesions of the eye, blindness, a reduction in central or peripheral vision, or a reduction in total vision. AB272763 to AB272953 represent sequences used in the exemplification of the present invention

Sequence 34 BP; 8 A; 9 C; 8 G; 0 T; 9 U; 0 Other;

Query Match 73.5%; Score 25; DB 10; Length 34;

Best Local Similarity 100.0%; Pred. No. 0.00058; Mismatches 0; Gaps 0;

Matches 25; Conservative 0; Indels 0; Gaps 0;

6 ACUGAUGAGCCGTCGCGGGAAC 30
6 ACUGAUGAGCCGTCGCGGGAAC 30

RESULT 15

AAC88594 AAC88594 standard; DNA; 44 BP.

AAC88594;

02-MAR-2001 (first entry)

Oligonucleotide #1 used to clone ribozyme SOD-1.295.

Ribozyme; retinal degradation; retinal disease; learning; memory; amyotrophic lateral sclerosis; tumour suppression; ss.

Mus sp.

MO200066780-A2.

09-NOV-2000.

28-APR-2000; 2000MO-US011509.

30-APR-1999; 99US-0131942P.

(UYFL) UNIV FLORIDA.

Lewin AS, Muzyczka N, Hauswirth WW, Teschendorf C, Burger C;

WPI; 2000-687548/67.

Novel methods for identifying genes with selected functions comprising contacting genes with a library of ribozymes, useful for identifying genes involved in, e.g. retinal disease, learning or memory and tumor suppression.

Example 7; Fig 36; 11pp; English.

The present invention relates to a method for identifying a gene with a selected function comprising contacting genes with a library of ribozymes and identifying at least 1 ribozyme that alters the selected function of the gene. The present sequence is an oligonucleotide used in the present invention. The methods (and ribozymes) are useful for identifying novel genes involved in retinal degradation, retinal disease, learning or memory, amyotrophic lateral sclerosis or tumour suppression, and for producing non-human animal models of diseases

XX Sequence 44 BP; 13 A; 11 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 73.5%; Score 25; DB 3; Length 44;

Best Local Similarity 84.0%; Pred. No. 0.00057; Mismatches 0; Gaps 0;

Matches 21; Conservative 4; Indels 0; Gaps 0;

6 ACUGAUGAGCCGTCGCGGGAAC 30
11 ACTGATGAGCCGTCGCGGGAAC 35

Search completed: August 28, 2006, 09:50:06
Job time : 286 secs

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GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:50:18 ; Search time 716 Seconds
(without alignments)
583.491 Million cell updates/sec

Title: US-09-847-601B-100

Perfect score: 34
Sequence: 1 ucgaacugaugagcgucgcggaacgaag 34

Scoring table: OLIGO_NTC
Gapop 60.0, Gapext 60.0

Searched: 18892170 seqs, 6143817638 residues

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Total number of hits satisfying chosen parameters: 37781012

Minimum DB seq length: 0

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16: /EMC_Celerra_SIDS3/pcodara/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	100.0	34	US-09-847-601B-100	Sequence 100, App
2	27	79.4	32	US-09-847-601B-101	Sequence 101, App
3	27	79.4	34	US-09-847-601B-98	Sequence 98, App
4	26	76.5	34	US-09-847-601B-92	Sequence 92, App
5	26	76.5	34	US-09-847-601B-93	Sequence 93, App
6	26	76.5	34	US-09-847-601B-99	Sequence 99, App
7	25	73.5	34	US-09-847-601B-90	Sequence 90, App
8	25	73.5	34	US-09-847-601B-91	Sequence 91, App
9	25	73.5	34	US-09-847-601B-95	Sequence 95, App
10	25	73.5	34	US-09-847-601B-96	Sequence 96, App
11	25	73.5	34	US-09-847-601B-97	Sequence 97, App
12	19	55.9	34	US-09-847-601B-94	Sequence 94, App
13	16	47.1	463	US-10-437-963-3252	Sequence 3252, App
14	16	47.1	1845	US-10-156-761-3619	Sequence 3619, App
15	16	47.1	5335	US-10-437-963-18859	Sequence 18859, App
16	16	47.1	6919	US-11-097-143-5630	Sequence 5630, App
17	16	47.1	9025608	US-10-156-761-1	Sequence 1, App

C 18	15	44.1	200	3	US-09-960-352-4463	Sequence 4463, App
C 19	15	44.1	250	3	US-09-864-761-31920	Sequence 31920, App
C 20	15	44.1	307	8	US-10-437-963-99234	Sequence 99234, App
C 21	15	44.1	343	9	US-10-425-115-36422	Sequence 36422, App
C 22	15	44.1	379	3	US-09-867-701-4078	Sequence 4078, App
C 23	15	44.1	389	4	US-09-925-065A-554407	Sequence 554407, App
C 24	15	44.1	389	5	US-09-925-065A-554407	Sequence 554407, App
C 25	15	44.1	522	8	US-10-282-122A-11370	Sequence 11370, App
C 26	15	44.1	573	3	US-09-864-761-15387	Sequence 15387, App
C 27	15	44.1	575	4	US-09-925-065A-637541	Sequence 637541, App
C 28	15	44.1	575	4	US-09-925-065A-637542	Sequence 637542, App
C 29	15	44.1	575	5	US-09-925-065A-637541	Sequence 637541, App
C 30	15	44.1	575	5	US-09-925-065A-637542	Sequence 637542, App
C 31	15	44.1	634	7	US-10-094-097B-106	Sequence 106, App
C 32	15	44.1	714	8	US-10-282-122A-14226	Sequence 14226, App
C 33	15	44.1	810	7	US-10-156-761-2123	Sequence 2123, App
C 34	15	44.1	852	8	US-10-282-122A-26469	Sequence 26469, App
C 35	15	44.1	873	8	US-10-282-122A-12733	Sequence 12733, App
C 36	15	44.1	939	7	US-10-156-761-4428	Sequence 4428, App
C 37	15	44.1	954	9	US-10-493-462-40	Sequence 40, App
C 38	15	44.1	957	8	US-10-282-122A-28269	Sequence 28269, App
C 39	15	44.1	974	6	US-10-198-846-13796	Sequence 13796, App
C 40	15	44.1	1155	6	US-10-309-515-9	Sequence 9, App
C 41	15	44.1	1155	7	US-10-126-764-9	Sequence 9, App
C 42	15	44.1	1401	8	US-10-181-906-5	Sequence 5, App
C 43	15	44.1	1413	3	US-09-815-242-6074	Sequence 6074, App
C 44	15	44.1	1413	7	US-10-369-493-24531	Sequence 24531, App
C 45	15	44.1	1413	8	US-10-282-122A-20379	Sequence 20379, App

ALIGNMENTS

RESULT 1
US-09-847-601B-100
Sequence 100, Application US/09847601B
Publication No. US2005096282A1
GENERAL INFORMATION:
APPLICANT: LEWIN, ALFRED S.
APPLICANT: SHAW, LYNN C.
TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
FILE REFERENCE: 4300, 014100
CURRENT APPLICATION NUMBER: US/09/847, 601B
CURRENT FILING DATE: 2001-05-01, 667
PRIOR APPLICATION NUMBER: 09/063, 667
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/046, 147
PRIOR FILING DATE: 1997-05-09
PRIOR APPLICATION NUMBER: 60/044, 492
PRIOR FILING DATE: 1997-04-21
NUMBER OF SEQ ID NOS: 162
SOFTWARE: Patent version 3.2
SEQ ID NO 100
LENGTH: 34
TYPE: RNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-100
Query Match 100.0%; Score 34; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.7e-10;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 UCgaacugaugagcgucgcggaacgaag 34
Db 1 ucgaacugaugagcgucgcggaacgaag 34
RESULT 2
US-09-847-601B-101

Sequence 101, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: SHAW, ALFRED S.
; APPLICANT: LEWIN, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 101
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601b-101

Query Match 79.4%; Score 27; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 AACUGAUGAGCCGUCGCGGCGAAACG 29

RESULT 3
US-09-847-601b-98
; Sequence 98, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601b-98

Query Match 79.4%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 5.7e-06;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGAAACG 31
Db 5 AACUGAUGAGCCGUCGCGGCGAAACG 31

RESULT 4
US-09-847-601b-92
; Sequence 92, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601b-92

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGAAAC 30
Db 5 AACUGAUGAGCCGUCGCGGCGAAAC 30

RESULT 5
US-09-847-601b-93
; Sequence 93, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT FILING DATE: 2001-05-01
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1998-04-21
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-05-09
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 93
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601b-93

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 AACUGAUGAGCCGUCGCGGCGAAAC 30

Db 5 AACUGAGAGCCGUCGCGGGAAC 30

RESULT 6

US-09-847-601B-99
; Sequence 99, Application US/09847601B
; Publication No. US2005096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 99
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-99

Query Match 76.5%; Score 26; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAGAGCCGUCGCGGGAAC 30
DB 5 AACUGAGAGCCGUCGCGGGAAC 30

RESULT 7
US-09-847-601B-90
; Sequence 90, Application US/09847601B
; Publication No. US2005096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-90

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGAGCCGUCGCGGGAAC 30
DB 6 ACUGAGAGCCGUCGCGGGAAC 30

RESULT 8

US-09-847-601B-91
; Sequence 91, Application US/09847601B
; Publication No. US2005096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-91

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGAGCCGUCGCGGGAAC 30
DB 6 ACUGAGAGCCGUCGCGGGAAC 30

RESULT 9
US-09-847-601B-95
; Sequence 95, Application US/09847601B
; Publication No. US2005096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-95

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 10

US-09-847-601B-96
; Sequence 96, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-96

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 11

US-09-847-601B-97
; Sequence 97, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial

FEATURE:
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-97

Query Match 73.5%; Score 25; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.1e-05;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
|||||
DB 6 ACUGAUGAGCCGUCGCGCGGAAC 30

RESULT 12

US-09-847-601B-94
; Sequence 94, Application US/09847601B
; Publication No. US20050096282A1
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/847,601B
; PRIOR FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 94
; LENGTH: 34
; TYPE: RNA
; ORGANISM: Artificial
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-847-601B-94

Query Match 55.9%; Score 19; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUCGCGCGGAAC 30
|||||
DB 12 GAGCCGUCGCGCGGAAC 30

RESULT 13

US-10-437-963-3252/c
; Sequence 3252, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 3252
; LENGTH: 463
; TYPE: DNA

ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_102953C.1
US-10-437-963-3252

Query Match 47.1%; Score 16; DB 8; Length 463;
Best Local Similarity 81.2%; Pred. No. 22;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 UGCAACTGAGGAGCC 16
DB 221 TGCMACTGATGAGCC 206

RESULT 14

US-10-156-761-3619
Sequence 3619, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3619
LENGTH: 1845
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1845)
US-10-156-761-3619

Query Match 47.1%; Score 16; DB 7; Length 1845;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUGCGGCGGA 27
DB 1633 GAGCCGTTGCGGCGGA 1648

RESULT 15

US-10-437-963-18859
Sequence 18859, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovacic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 18859

LENGTH: 5335
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(5335)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_24377C.1
US-10-437-963-18859

Query Match 47.1%; Score 16; DB 8; Length 5335;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUGCGGCGGA 27
DB 352 GAGCCGTTGCGGCGGA 367

Search completed: August 28, 2006, 10:41:09
Job time : 718 secs

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OM nucleic - nucleic search, using SW model

Run on: August 28, 2006, 09:54:05 ; Search time 780 Seconds
(without alignments)
71.045 Million cell updates/sec

Title: US-09-847-601b-100

Sequence: 1 ucgaacgaugagcgucgucgagcggaacgaag 34

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Searched: 2239192 seqs, 814926892 residues

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Total number of hits satisfying chosen parameters: 4478184

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database: Published Applications NA New:

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2: /EMC Celerra SIDS3/ptodata/1/pubpna/US06 NEW PUB.seq:*
3: /EMC Celerra SIDS3/ptodata/1/pubpna/US07 NEW PUB.seq:*
4: /EMC Celerra SIDS3/ptodata/1/pubpna/US08 NEW PUB.seq:*
5: /EMC Celerra SIDS3/ptodata/1/pubpna/PCT_NEW PUB.seq:*
6: /EMC Celerra SIDS3/ptodata/1/pubpna/US10 NEW PUB.seq:*
7: /EMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq:*
8: /EMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq1:*
9: /EMC Celerra SIDS3/ptodata/1/pubpna/US11 NEW PUB.seq2:*
10: /EMC Celerra SIDS3/ptodata/1/pubpna/US60 NEW PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	47.1	1809	US-10-449-902-27861	Sequence 27861, A
2	15	44.1	1084	US-11-266-748A-184169	Sequence 184169, A
3	15	44.1	1084	US-11-266-748A-191642	Sequence 191642, A
4	15	44.1	1155	US-11-266-748A-25135	Sequence 25135, A
5	15	44.1	1243	US-10-449-902-20318	Sequence 20318, A
6	15	44.1	1249	US-10-449-902-4455	Sequence 4455, Ap
7	15	44.1	1342	US-11-266-748A-251890	Sequence 251890, A
8	15	44.1	1342	US-11-266-748A-312407	Sequence 312407, A
9	15	44.1	1551	US-10-449-902-20725	Sequence 20725, A
10	15	44.1	1773	US-11-266-748A-184170	Sequence 184170, A
11	15	44.1	2253	US-11-266-748A-191643	Sequence 191643, A
12	15	44.1	2253	US-11-266-554-73	Sequence 73, Ap1
13	15	44.1	2752	US-11-248-718-73	Sequence 73, Ap1
14	15	44.1	2775	US-11-266-748A-29125	Sequence 29125, A
15	15	44.1	3309	US-10-449-902-15931	Sequence 15931, A
16	15	44.1	3389	US-10-449-902-22857	Sequence 22857, A
17	15	44.1	3389	US-11-248-305-16426	Sequence 16426, A
18	15	44.1	611	US-11-266-748A-362168	Sequence 362168, A
19	15	41.2	611	US-11-266-748A-445547	Sequence 445547, A
20	15	41.2	620	US-11-266-748A-6564	Sequence 6564, Ap
21	15	41.2	642	US-11-266-748A-98682	Sequence 98682, A
22	15	41.2	642	US-11-266-748A-151493	Sequence 151493, A
23	15	41.2	642	US-11-266-748A-151493	Sequence 151493, A

ALIGNMENTS

C	24	14	41.2	777	8	US-11-266-748A-174235	Sequence 174235, A
C	25	14	41.2	777	8	US-11-266-748A-190325	Sequence 190325, A
C	26	14	41.2	795	9	US-11-056-355B-78299	Sequence 78299, A
C	27	14	41.2	820	8	US-11-266-748A-189268	Sequence 189268, A
C	28	14	41.2	918	8	US-11-266-748A-352337	Sequence 352337, A
C	29	14	41.2	918	8	US-11-266-748A-435716	Sequence 435716, A
C	30	14	41.2	1169	6	US-10-449-902-11462	Sequence 11462, A
C	31	14	41.2	1229	6	US-10-520-999-5	Sequence 5, Ap1
C	32	14	41.2	1229	6	US-10-520-999-4	Sequence 4, Ap1
C	33	14	41.2	1253	6	US-10-520-999-1	Sequence 1, Ap1
C	34	14	41.2	1280	6	US-10-520-999-3	Sequence 3, Ap1
C	35	14	41.2	1602	6	US-10-520-999-2	Sequence 2, Ap1
C	36	14	41.2	1817	6	US-10-471-571A-4927	Sequence 4927, Ap
C	37	14	41.2	1937	9	US-11-216-545-3254	Sequence 3254, Ap
C	38	14	41.2	2031	9	US-11-218-305-10001	Sequence 10001, A
C	39	14	41.2	2043	6	US-10-520-999-6	Sequence 6, Ap1
C	40	14	41.2	2638	9	US-11-218-305-13290	Sequence 13290, A
C	41	14	41.2	3134	9	US-11-218-305-10002	Sequence 10002, A
C	42	14	41.2	3786	6	US-10-473-173-28	Sequence 28, Ap1
C	43	14	41.2	4009	8	US-11-266-748A-24493	Sequence 24493, A
C	44	14	41.2	5514	8	US-11-266-748A-30117	Sequence 30117, A
C	45	14	41.2	5964	8	US-11-266-748A-28460	Sequence 28460, A

RESULT 1
US-10-449-902-27861
Sequence 27861, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: Foundation for Advancement of International Science.
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ. ID NOS: 56791
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 27861
LENGTH: 1809
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK103303
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-27861

Query Match 47.1%; Score 16; DB 6; Length 1809;
Best Local Similarity 87.5%; Pred. No. 2.7;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGUCGCGCGA 27
DB 537 GAGCCGTCGCGCGA 552

RESULT 2
US-11-266-748A-184169
Sequence 184169, Application US/11266748A
Publication No. US20060134653A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Transcriptome Microarray Technology and

```

; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 60/700,293
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 184169
; LENGTH: 1084
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-184169

Query Match      44.1%; Score 15; DB 8; Length 1084;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy      6 ACUGAUGAGCCGCTTC 20
Db      736 ACTGATGAGCCGCTTC 750

RESULT 3
US-11-266-748A-191642
; Sequence 191642, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harrin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191642
; LENGTH: 1084
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-191642
```

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Query Match      44.1%; Score 15; DB 8; Length 1084;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy      6 ACUGAUGAGCCGCTTC 20
Db      736 ACTGATGAGCCGCTTC 750

RESULT 4
US-11-266-748A-25135
; Sequence 25135, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harrin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; TITLE OF INVENTION: Methods of Using the Same
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: EP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105507.0
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25135
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-25135

Query Match      44.1%; Score 15; DB 8; Length 1155;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Oy      6 ACUGAUGAGCCGCTTC 20
Db      538 ACTGATGAGCCGCTTC 552

RESULT 5
US-10-449-902-20318
; Sequence 20318, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
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NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20318
LENGTH: 1243
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK099148
DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-20318

Query Match 44.1% Score 15; DB 6; Length 1243;
Best Local Similarity 86.7% Pred. No. 11;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAACUGAGGACC 16
DB 390 GCAACUGAGGACC 404

RESULT 6

US-10-449-902-4455
Sequence 4455, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Science.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4455
LENGTH: 1249
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK061781
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-4455

Query Match 44.1% Score 15; DB 6; Length 1249;
Best Local Similarity 86.7% Pred. No. 11;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAACUGAGGACC 16
DB 405 GCAACUGAGGACC 419

RESULT 7

US-11-266-748A-251890/C
Sequence 251890, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Hartin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 251890
LENGTH: 1342
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-251890

Query Match 44.1% Score 15; DB 8; Length 1342;
Best Local Similarity 73.3% Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGGCGGUC 20
DB 318 ACUGAGGCGGUC 304

RESULT 8

US-11-266-748A-312407
Sequence 312407, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Hartin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcription Microarray Technology and
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 48396
SOFTWARE: PatentIn version 3.3
SEQ ID NO 312407
LENGTH: 1342
TYPE: DNA
ORGANISM: Homo Sapiens
US-11-266-748A-312407

Query Match 44.1% Score 15; DB 8; Length 1342;
Best Local Similarity 73.3% Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAGGCGGUC 20
DB 318 ACUGAGGCGGUC 304

Db 1025 ACTGATGAGCCGTTT 1039

RESULT 9

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US-10-449-902-20725
Sequence 20725, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented technology Research Advancement Institution
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 20725
LENGTH: 1551
TYPE: DNA
ORGANISM: Oryza sativa
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AK071031
DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-20725

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Query Match Similarity	44.1%	Score 15;	DB 6;	Length 1551;
Best Local Similarity	86.7%	Pred. No. 11;		
Matches 13; Conservative	2;	Mismatches	0;	Gaps 0;

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QY      14 GCCGUTC GCCGCGAA 28
          |||::|||
Db      291 GCCGTCGCCGCGAA 305

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RESULT 10

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US-11-256-428-61/c
/ Sequence 61, Application US/11256428
/ Publication No. US20060095987A1
/ GENERAL INFORMATION:
/ APPLICANT: Niblett, Charles L.
/ TITLE OF INVENTION: Methods and Materials for Conferring Resistance to Pests and
/ TITLE OF INVENTION: Pathogens of Plants
/ FILE REFERENCE: VEN-100
/ CURRENT APPLICATION NUMBER: US/11/256,428
/ CURRENT FILING DATE: 2005-10-21
/ NUMBER OF SEQ ID NOS: 69
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 61
/ LENGTH: 1773
/ TYPE: DNA
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Pratylenchus scribneri rDNA
/ US-11-256-428-61

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Query Match Similarity	44.1%;	Score 15:	DB 8;	Length 1773;
Best Local Similarity	80.0%;	Pred. No. 11;		
Matches 12; Conservative	3;	Mismatches	0;	Indels 0; Gaps 0;

QY	10	AUGAGCCG	UUCGCGG	24
		:	: :	
Db	72	ATGAGCCG	TTGCGGG	58

RESULT 11

US-11-266-748A-184170
Sequence 184170, Application US/11266748A

Publication No. US20060134663A1

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1  GENERAL INFORMATION:
2  APPLICANT: Harkin, Paul
3  APPLICANT: Johnson, Patrick
4  APPLICANT: Mulligan, Karl
5  TITLE OF INVENTION: Transcriptome Microarray Technology and
6  TITLE OF INVENTION: Methods of Using the Same
7  FILE REFERENCE: 55815-.0102 (319189)
8  CURRENT APPLICATION NUMBER: US/11/266,748A
9  CURRENT FILING DATE: 2005-11-03
10 PRIOR APPLICATION NUMBER: EP 04105479.2
11 PRIOR FILING DATE: 2004-11-03
12 PRIOR APPLICATION NUMBER: EP 04105482.6
13 PRIOR FILING DATE: 2004-11-03
14 PRIOR APPLICATION NUMBER: EP 04105483.4
15 PRIOR FILING DATE: 2004-11-03
16 PRIOR APPLICATION NUMBER: EP 04105507.0
17 PRIOR FILING DATE: 2004-11-03
18 PRIOR APPLICATION NUMBER: EP 04105485.9
19 PRIOR FILING DATE: 2004-11-03
20 PRIOR APPLICATION NUMBER: EP 04105484.2
21 PRIOR FILING DATE: 2004-11-03
22 PRIOR APPLICATION NUMBER: US 60/662,276
23 PRIOR FILING DATE: 2005-03-14
24 PRIOR APPLICATION NUMBER: US 60/700,293
25 PRIOR FILING DATE: 2005-07-18
26 NUMBER OF SEQ ID NOS: 483996
27 SOFTWARE: PatentIn version 3.3
28 SEQ ID NO 184170
29 LENGTH: 2253
30 TYPE: DNA
31 ORGANISM: Homo Sapiens
32 FEATURE:
33 NAME/KEY: misc feature
34 LOCATION: (2038)..(2071)
35 OTHER INFORMATION: n is a, c, g, or t
36
37 -S-11-266-748A-184170

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Query Match	44.1%;	Score 15;	DB 8;	Length 2253;
Best Local Similarity	73.3%;	Pred. No. 11;		
Matches 11; Conservative	4;	Mismatches 0;	Indels 0;	Gaps 0;

2y 6 ACTGAUGAGCCCGTUC 20
 ||:|||||:|:
 Db 796 ACTGATGAGCCGTTTC 810

RESULT 12

US-11-266-748A-1916A3
Sequence 1916A3, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266, 748A
PRIORITY FILING DATE: 2005-11-03
PRIORITY APPLICATION NUMBER: EP 04105479.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105482.6
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105483.4
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105507.0
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105485.9
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: EP 04105484.2
PRIORITY FILING DATE: 2004-11-03
PRIORITY APPLICATION NUMBER: US 60/662, 276

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; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 191643
; LENGTH: 2253
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2038)..(2071)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-191643
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Query Match          44.1%  Score 15; DB 8; Length 2253;
Best Local Similarity 73.3%  Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy          6  ACUGAUGAGCCGCTTC 20
Db          796  ACTGATGAGCCGCTTC 810
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RESULT 13
US-11-226-554-73
; Sequence 73, Application US/11226554
; Publication No. US20060147373A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; FILE REFERENCE: P5001R1
; CURRENT APPLICATION NUMBER: US/11/226,554
; PRIOR FILING DATE: 2005-09-13/17,488
; PRIOR APPLICATION NUMBER: US 10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 73
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-226-554-73
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Query Match          44.1%  Score 15; DB 9; Length 2752;
Best Local Similarity 73.3%  Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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Qy          6  ACUGAUGAGCCGCTTC 20
Db          746  ACTGATGAGCCGCTTC 760
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RESULT 14
US-11-248-718-73
; Sequence 73, Application US/11248718
; Publication No. US20060160997A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
```

```

; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; FILE REFERENCE: P5001R1 US
; CURRENT APPLICATION NUMBER: US/11/248,718
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/336,827
; PRIOR FILING DATE: 2001-11-07
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 73
; LENGTH: 2752
; TYPE: DNA
; ORGANISM: Homo Sapien
US-11-248-718-73
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Query Match          44.1%  Score 15; DB 9; Length 2752;
Best Local Similarity 73.3%  Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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```
Qy          6  ACUGAUGAGCCGCTTC 20
Db          746  ACTGATGAGCCGCTTC 760
```

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RESULT 15
US-11-266-748A-29125
; Sequence 29125, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Johnston, Patrick
; APPLICANT: Mulligan, Karl
; TITLE OF INVENTION: Transcription Microarray Technology and
; FILE REFERENCE: 55815-0102 (319189)
; CURRENT APPLICATION NUMBER: US/11/266,748A
; PRIOR FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: BP 04105479.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: BP 04105482.6
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: BP 04105483.4
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: BP 04105507.0
; PRIOR FILING DATE: 2004-11-03
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; PRIOR APPLICATION NUMBER: EP 04105485.9
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: EP 04105484.2
; PRIOR FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US 60/662,276
; PRIOR FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/700,293
; PRIOR FILING DATE: 2005-07-18
; NUMBER OF SEQ ID NOS: 483996
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29125
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-11-266-748A-29125
```

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Query Match 44.1%; Score 15; DB 8; Length 2775;
Best Local Similarity 73.3%; Pred. No. 11;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
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OY 6 ACUGAUGAGCCGUC 20
||:|||||:|
Db 804 ACTGATGAGCCGTC 818
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Search completed: August 28, 2006, 10:07:13
Job time : 781 secs

GenCore version 5.1.9
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OW nucleic - nucleic search, using sw model

Run on: August 28, 2006, 09:45:17 ; Search time 2332 Seconds
(without alignments)
815.290 Million cell updates/sec

Title: US-09-847-601b-100

Perfect score: 34
Sequence: 1 ucgaacugagagccgucgcgcgaacgaag 34

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 48236798 seqs, 27959665780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96473154

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST: *
1: gb_est1: *
2: gb_est3: *
3: gb_est4: *
4: gb_est5: *
5: gb_est6: *
6: gb_hic: *
7: gb_est2: *
8: gb_est7: *
9: gb_est8: *
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11: gb_gsa1: *
12: gb_gsa2: *
13: gb_gsa3: *
14: gb_gsa4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18	52.9	470	1	AV681631
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4	18	52.9	592	13	CZ820348 OC_Ba017
5	18	52.9	660	13	CZ804464 OC_Ba017
6	18	52.9	910	13	CZ878583 OC_Ba028
7	17	50.0	591	14	DU808944 OG_Aba009
8	17	50.0	666	13	CL554761 OB_Ba000
9	17	50.0	738	14	DU660702 OG_Aba006
10	17	50.0	763	14	DX010184 OG_Aba011
11	17	50.0	795	14	DX290906 OR_Aba019
12	17	50.0	904	13	CM785911 SP_Ba001
13	17	50.0	955	14	DU759063 ASNG2280.
14	17	50.0	1299	12	BZ692135 SP_Ba001
15	16	47.1	359	4	BM686335
16	16	47.1	367	4	BM805921
17	16	47.1	456	10	N71828
18	16	47.1	515	11	AZ928987
19	16	47.1	518	13	CZ727431

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C 21	16	47.1	522	8	CV095014	CV095014 FAMU USDA
C 22	16	47.1	588	4	BX333850	BX333850 B333850
C 23	16	47.1	657	13	CZ178899	CZ178899 MIRA-BA04
C 24	16	47.1	730	14	AG325093	AG325093 Mus muscu
C 25	16	47.1	779	5	CF208340	CF208340 CAB20003
C 26	16	47.1	794	5	CF287058	CF287058 AGNCOURT
C 27	16	47.1	811	14	CNS04Q59	AL302994 Tetradon
C 28	16	47.1	839	8	CV214664	CV214664 EST874374
C 29	16	47.1	874	10	DV006952	DV006952 CNB243-H0
C 30	16	47.1	907	8	CO023557	CO023557 EST819650
C 31	16	47.1	946	7	AM155158	AM155158 mg1e0002G
C 32	16	47.1	1083	13	CM929167	CM929167 EDCBV35TR
C 33	16	47.1	1120	9	DR140280	DR140280 49191388
C 34	15	44.1	64	7	AM626734	AM626734 SMOVAFAP
C 35	15	44.1	73	4	CB832373	CB832373 SMDmFCAY
C 36	15	44.1	73	7	AM651879	AM651879 SMD25CAN
C 37	15	44.1	80	8	CO653412	CO653412 081a01b H
C 38	15	44.1	106	1	AA547823	AA547823 MB3D6V1D0
C 39	15	44.1	119	1	A1058040	A1058040 SMDMCA12
C 40	15	44.1	145	2	BM033558	BM033558 kb65e12.Y
C 41	15	44.1	155	14	AJ622806	AJ622806 Drosophila
C 42	15	44.1	177	4	CB856215	CB856215 r149f02.Y
C 43	15	44.1	178	1	AA509306	AA509306 MBAFCX960
C 44	15	44.1	210	2	BI783608	BI783608 kb35e02.Y
C 45	15	44.1	216	7	AM043480	AM043480 SWI4CAK01

ALIGNMENTS

RESULT 1
LOCUS CZ820350
DEFINITION OC_Ba0198H18.r OC_Ba Oryza coarctata genomic clone OC_Ba0198H18
3', genomic survey sequence.
ACCESSION CZ820350
VERSION
KEYWORDS
SOURCE
ORGANISM
GSS.
Oryza coarctata (Porteresia coarctata) -
Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D., Rao,K., Luo,M., Jettly,R., Kudrna,D., Muller,C., Soderlund,C. and Wing,R.
TITLE OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
JOURNAL Unpublished (2005)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rtwing@genome.arizona.edu

FEATURES
source
1..311
Location/Qualifiers
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0198H18"
/cfeature="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_11b="OC_Ba"

ORIGIN /note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

Query Match 52.9%; Score 18; DB 13; Length 311;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 UGAGCCGUTCGCGCGAA 28
:|||||:|||||
Db 225 TGAGCCGTTCCGCGCGAA 242

RESULT 2
AV681631 470 bp mRNA linear EST 16-JAN-2002
LOCUS AV681631 GKB Homo sapiens cDNA clone GKBAJH02 5', mRNA sequence.
DEFINITION AV681631
ACCESSION AV681631 GI:10283494
VERSION
KEYWORDS EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo
1 (bases 1 to 470)
Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X.,
Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X.,
Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
1..470
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GKBAJH02"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_1lb="GKB"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 52.9%; Score 18; DB 1; Length 470;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 14; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AAACGAGGAGCCGTCG 21
:|||||:|||||
Db 273 AAACGAGGAGCCGTCG 230

RESULT 3
CZ802927 579 bp DNA linear GSS 26-JUL-2005
LOCUS CZ802927
DEFINITION OC_Ba0175A06.f OC_Ba Oryza coarctata genomic clone OC_Ba0175A06
5', genomic survey sequence.
ACCESSION CZ802927
VERSION CZ802927.1 GI:71242780
KEYWORDS GSS.

SOURCE Oryza coarctata (Porteresia coarctata)

ORGANISM Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 579)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0175 row: A column: 06
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends

FEATURES
Location/Qualifiers
1..579
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0175A06"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1lb="OC_Ba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 579;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 UGAGCCGUTCGCGCGAA 28
:|||||:|||||
Db 440 TGAGCCGTTCCGCGCGAA 457

RESULT 4
CZ820348 592 bp DNA linear GSS 26-JUL-2005
LOCUS CZ820348
DEFINITION OC_Ba0198H17.r OC_Ba Oryza coarctata genomic clone OC_Ba0198H17
3', genomic survey sequence.
ACCESSION CZ820348
VERSION CZ820348.1 GI:71260201
KEYWORDS GSS.
SOURCE Oryza coarctata (Porteresia coarctata)
ORGANISM Oryza coarctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 592)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0198 row: H column: 17
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
Source
Location/Qualifiers
1..592

/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0198H17"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1lb="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 52.9%; Score 18; DB 13; Length 592;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
OY 11 UGAGCCGUCGCGCGCA 28
:|||||:|||||
Db 253 TGAGCCGTCGCGCGCA 270

RESULT 5
CZ804464 660 bp DNA linear GSS 26-JUN-2005
LOCUS OC_Ba0177B01.f OC_Ba Oryza coarctata genomic clone OC_Ba0177B01
DEFINITION 5', genomic survey sequence.
ACCESSION CZ804464 GI:71244317
VERSION GSS.
KEYWORDS Oryza coarctata (Porteresia coarctata)
SOURCE Oryza coarctata
ORGANISM Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 660)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0177 row: B column: 01
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
1..660

FEATURES
Source
Location/Qualifiers
1..660
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0177B01"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1lb="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN
Query Match 52.9%; Score 18; DB 13; Length 660;

Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 11 UGAGCCGUCGCGCGCA 28
:|||||:|||||
Db 228 TGAGCCGTCGCGCGCA 245

RESULT 6
CZ878583 910 bp DNA linear GSS 27-JUN-2005
LOCUS OC_Ba0280C17.f OC_Ba Oryza coarctata genomic clone OC_Ba0280C17
DEFINITION 5', genomic survey sequence.
ACCESSION CZ878583
VERSION GSS.
KEYWORDS Oryza coarctata (Porteresia coarctata)
SOURCE Oryza coarctata
ORGANISM Oryza coarctata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 910)
Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0280 row: C column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
1..910

FEATURES
Source
Location/Qualifiers
1..910
/organism="Oryza coarctata"
/mol_type="genomic DNA"
/db_xref="taxon:77588"
/clone="OC_Ba0280C17"
/tissue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_1lb="OC_Ba"
/note="Vector: PAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN
Query Match 52.9%; Score 18; DB 13; Length 910;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 15; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 11 UGAGCCGUCGCGCGCA 28
:|||||:|||||
Db 437 TGAGCCGTCGCGCGCA 454

RESULT 7
DU808944 591 bp DNA linear GSS 13-DEC-2005
LOCUS OG_ABa0093B05.r OG_ABa Oryza granulata genomic clone OG_ABa0093B05
DEFINITION 3', genomic survey sequence.
ACCESSION DU808944 GI:83604603
VERSION GSS.
KEYWORDS Oryza granulata
SOURCE Oryza granulata
ORGANISM Oryza granulata
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

ORIGIN
Query Match 52.9%; Score 18; DB 13; Length 591;

REFERENCE
AUTHORS

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.

TITLE
JOURNAL
COMMENT

1 (bases 1 to 591)
SamMiguel,P., Westerman,R., Kim,H., Yu,Y., Wiscocki,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.,
OMAP (Oryza Map Alignment Project) - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu

FEATURES

Query Match 50.0%; Score 17; DB 14; Length 591;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Bases 107-697 of the raw sequence (length 1052) were retained after
clipping.
Plate: 0093 row: E column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

SOURCE

location/Qualifiers
1..591
/organism="Oryza granulata"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OG_Aba0093E05"
/issue_type="Young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OG_Aba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 50.0%; Score 17; DB 14; Length 591;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Bases 107-697 of the raw sequence (length 1052) were retained after
clipping.
Plate: 0093 row: E column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

RESULT 8
LOCUS
DEFINITION
VERSION
KEYWORDS
SOURCE
ORGANISM

CL554761 666 bp DNA linear GSS 14-JUN-2004
OB_Ba0004E01.f OB_Ba Oryza brachyantha genomic clone
OB_Ba0004E01 5', genomic survey sequence.
CL554761
GSS.
GI:47632656

TITLE
JOURNAL
COMMENT

Oryza brachyantha
Oryza brachyantha
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 666)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 625 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 145000 Std Error: 0.00
Plate: 0004 row: E column: 01

FEATURES
SOURCE

Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
location/Qualifiers
1..666
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OB_Ba0004E01"
/issue_type="leaves"
/dev_stage="mature"
/lab_host="DH10B"
/clone_lib="OB_Ba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

ORIGIN

Query Match 50.0%; Score 17; DB 13; Length 666;
Best Local Similarity 88.2%; Pred. No. 47;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Bases 107-697 of the raw sequence (length 1052) were retained after
clipping.
Plate: 0093 row: E column: 05
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

SOURCE

location/Qualifiers
1..666
/organism="Oryza brachyantha"
/mol_type="genomic DNA"
/db_xref="taxon:110450"
/clone="OG_Aba0063J17"
/issue_type="Young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OG_Aba"
/note="Vector: pAGIBAC1, Site_1: HindIII, Site_2: HindIII"

REFERENCE
AUTHORS

1 (bases 1 to 738)
SamMiguel,P., Westerman,R., Kim,H., Yu,Y., Wiscocki,M., Yost,D.,
Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C.,
Hatfield,J., Soderlund,C., Wing,R. and Jackson,S.A.,
OMAP (Oryza Map Alignment Project) - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson
Jackson Laboratory
Purdue University
915 W. State St., West Lafayette, IN 47907, USA
Tel: 7654963621
Fax: 7654967255
Email: sjackson@purdue.edu

TITLE
JOURNAL
COMMENT

Oryza granulata
Oryza granulata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 738)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 625 9595
Fax: 520 621 1259
Email: twing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert length: 145000 Std Error: 0.00
Plate: 0004 row: E column: 01

QY 12 GAGCCGTCGCGCGCAA 28
 DB 588 GAGCCGTCGCGCGCAA 604

RESULT 10
 DX010184
 LOCUS
 DEFINITION OG_Aba0110K10.f OG_Aba Oryza granulata genomic clone OG_Aba0110K10
 5', genomic survey sequence.
 ACCESSION DX010184 GI:84416351
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza granulata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 OMAP (Oryza Map Alignment Project) - Purdue University
 Unpublished (2004)
 Contact: Scott A. Jackson
 Jackson Laboratory
 Purdue University
 915 W. State St., West Lafayette, IN 47907, USA
 Tel: 765/4963621
 Fax: 765/4967255
 Email: sjackson@purdue.edu
 HindIII (presumptive cloning site) found. Basecalling by phred
 version 0.020425.c. This sequence was derived from the raw sequence
 read by clipping with Lucy version 1.19s. Bases 31-793 of the raw
 sequence (length 1065) were retained after clipping.
 Plate: 0110 row: K column: 10
 Seq primer: TAA TAC GAC TCA CTA TAG GG
 Class: BAC ends.

FEATURES
 source
 location/Qualifiers
 1..763
 /organism="Oryza granulata"
 /mol_type="genomic DNA"
 /db_xref="taxon:110450"
 /clone="OG_Aba0110K10"
 /tissue_type="young leaves"
 /lab_host="DH10B T1 phage resistant"
 /clone_1lb="OG_Aba"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
 Query Match 50.0%; Score 17; DB 14; Length 763;
 Best Local Similarity 88.2%; Pred. No. 47;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGTCGCGCGCAA 28
 DB 315 GAGCCGTCGCGCGCAA 331

RESULT 11
 DX290906 795 bp DNA linear GSS 20-JAN-2006
 LOCUS
 DEFINITION OR_Aba0194J18.f OR_Aba Oryza riddlei genomic clone OR_Aba0194J18
 5', genomic survey sequence.
 ACCESSION DX290906 GI:85561663
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza riddlei
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
 clade; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute
 Unpublished (2005)
 Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 Plate: 0194 row: J column: 18
 Class: BAC ends.

FEATURES
 source
 location/Qualifiers
 1..795
 /organism="Oryza riddlei"
 /mol_type="genomic DNA"
 /db_xref="taxon:83308"
 /clone="OR_Aba0194J18"
 /tissue_type="leaves"
 /lab_host="DH10B"
 /clone_1lb="OR_Aba"
 /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
 Query Match 50.0%; Score 17; DB 14; Length 795;
 Best Local Similarity 88.2%; Pred. No. 47;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 GAGCCGTCGCGCGCAA 28
 DB 238 GAGCCGTCGCGCGCAA 254

RESULT 12
 CW785911 904 bp DNA linear GSS 22-NOV-2004
 LOCUS
 DEFINITION SP_Ba0016N09.r SP_Ba Sorghum prolingum genomic clone
 SP_Ba0016N09 3', genomic survey sequence.
 ACCESSION CW785911 GI:55927805
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Sorghum prolingum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
 AUTHORS
 Bowers, J.E., Arias, M.A., Asher, R., Avise, J.A., Ball, R.T.,
 Brewer, G.A., Bues, R.W., Chen, A.H., Edwards, T.M., Estill, J.C.,
 Eum, H.B., Goff, V.H., Herrick, K.L., Steele, C.L., Karunakaran, S.,
 Lafayette, G.K., Lemke, C., Marler, B.S., Masters, S.L., McMillan, J.M.,
 Nelson, L.K., Newsome, G.A., Nwankema, C.C., Odoh, R.N., Phelps, C.A.,
 Rarick, E.A., Rogers, C.J., Ryan, S.P., Slaughter, K.A.,
 Soderlund, C.A., Tang, H., Wing, R.A., and Peterson, A.H.
 Comparative physical mapping links conservation of microsatellite to
 chromosome structure and recombination in grasses
 Proc. Natl. Acad. Sci. U.S.A. 102 (37), 13206-13211 (2005)
 16141333
 Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 PCR Primers
 FORWARD: TAA TAC GAC TCA CTA TAG GG
 BACKWARD: CAC TCA TTA GCG ACC CCA
 Plate: 0016 row: N column: 09
 Seq primer: CAC TCA TTA GCG ACC CCA
 Class: BAC ends.

FEATURES

Source

Location/Qualifiers
1. .904
/organism="Sorghum propinquum"
/mol_type="genomic DNA"
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HindIII; Paterson lab BAC library (HindIII)"

ORIGIN

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Best Local Similarity 76.5%; Pred. No. 47;
Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19
||||:||||:||||:
Db 768 CAAACTGATGAGCCGTT 752

RESULT 13 955 bp DNA linear GSS 27-JAN-2006
DUT59063
LOCUS ASNG2280.g2 HF200_10-06-02 uncultured marine microorganism
DEFINITION HF200_10-06-02 genomic clone HF200_082H09, genomic survey

ACCESSION

DUT59063

VERSION DUT59063

KEYWORDS GSS.

SOURCE unclutered marine microorganism HF200_10-06-02

ORGANISM unclutered marine microorganism HF200_10-06-02

REFERENCE 1 (bases 1 to 955)

AUTHORS Delong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,

Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.

and Karl,D.M.

Comparative genomics reveals ecological trends in stratified

microbial communities in the ocean's interior

Science (2006) In press

Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,

Kerrie Barry, Tjiana Glavinadelrio, David Bruce, Paul Richardson

and Edward Delong

US DOE Joint Genome Institute

US DOE Joint Genome Institute

2800 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA

Tel: 617-253-5271

Fax: 617-253-2679

Email: pwrichardson@lbl.gov; delong@mit.edu

North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid

DNA library prepared from marine picoplankton in the less than 1.6

um, greater than 0.22 um fraction. Sample Date: 10/6/2002

Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C

Salinity: 35.04 psu Oxygen: 198.8 umol/kg

Class: fosmid ends.

Location/Qualifiers

1. .955

/organism="uncultured marine microorganism HF200_10-06-02"

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/clone="HF200_082H09"

/cell_type="marine picoplankton, less than 1.8 um, greater

than 0.22 um fraction"

/clone_lib="HF200_10-06-02"

/note="Vector: pCC1FOS; North Pacific Subtropical Gyre

(Hawaii) picoplankton genomic fosmid DNA library prepared

from marine picoplankton in the less than 1.6 um, greater

than 0.22 um fraction. Picoplankton collected at 200 m

depth on 10/6/2002, Coordinates: 22.45 N, 158 W Depth 200 m

Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8

umol/kg"

ORIGIN

Query Match 50.0%; Score 17; DB 14; Length 955;

Best Local Similarity 82.4%; Pred. No. 47;

Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GAUGAGCCGUCGCGGC 25

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Db 273 GATGAGCCGTTCCGCGC 289

RESULT 14 1299 bp DNA linear GSS 02-JUL-2003

B2692135/c

LOCUS SP_Ba0016N09.r SP_Ba Sorghum propinquum genomic clone

DEFINITION SP_Ba0016N09 3, genomic survey sequence.

ACCESSION B2692135

VERSION B2692135

KEYWORDS GSS.

SOURCE Sorghum propinquum

ORGANISM Sorghum propinquum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 1299)

AUTHORS Wang,R., Yu,Y., Kim,H.R., Collura,K., Pries,G., Currie,J.,

Soderlund,C. and Hatfield,J.

Sequencing of Sorghum BAC ends.

http://genome.arizona.edu/stc/sorghum

Unpublished (2003)

Contact: Rod Wang

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rtwing@genome.arizona.edu

PCR Primers

FORWARD: atc agc ggc cgc gat cc

BACKWARD: gta aac cga cgg cca gtc

Plate: 0016 row: N column: 09

Seq primer: gta aac cga cgg cca gtc

Class: BAC ends.

Location/Qualifiers

1. .1299

/organism="Sorghum propinquum"

/mol_type="genomic DNA"

/db_xref="taxon:132711"

/clone="SP_Ba0016N09"

/clone_lib="SP_Ba"

/note="Vector: pBelBAC11, Site_1: HindIII, Site_2:

HindIII; Paterson lab BAC library (HindIII)"

ORIGIN

Query Match 50.0%; Score 17; DB 12; Length 1299;

Best Local Similarity 76.5%; Pred. No. 47;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19

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Db 801 CAAACTGATGAGCCGTT 785

RESULT 15 359 bp mRNA linear EST 07-NOV-2005

BW868335

LOCUS BW868335 Amphioxus Branchiostoma floridae unpublished cDNA library,

neurula whole animal Branchiostoma floridae cDNA clone dfne085101

5', mRNA sequence.

ACCESSION BW868335

VERSION BW868335

KEYWORDS EST.

SOURCE Branchiostoma floridae (Florida lancelet)

ORGANISM Branchiostoma floridae

ORIGIN

Query Match 50.0%; Score 17; DB 13; Length 904;

Best Local Similarity 76.5%; Pred. No. 47;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19

||||:||||:||||:
Db 768 CAAACTGATGAGCCGTT 752

RESULT 13 955 bp DNA linear GSS 27-JAN-2006

DUT59063

LOCUS ASNG2280.g2 HF200_10-06-02 uncultured marine microorganism

DEFINITION HF200_10-06-02 genomic clone HF200_082H09, genomic survey

ACCESSION DUT59063

VERSION DUT59063

KEYWORDS GSS.

SOURCE unclutered marine microorganism HF200_10-06-02

ORGANISM unclutered marine microorganism HF200_10-06-02

REFERENCE 1 (bases 1 to 955)

AUTHORS Delong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,

Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.

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North Pacific Subtropical Gyre (Hawaii) picoplankton genomic fosmid

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Coordinates: 22.45 N, 158 W Depth 200 m Temperature: 18.53 C

Salinity: 35.04 psu Oxygen: 198.8 umol/kg

Class: fosmid ends.

Location/Qualifiers

1. .955

/organism="uncultured marine microorganism HF200_10-06-02"

/mol_type="genomic DNA"

/db_xref="taxon:1361147"

/clone="HF200_082H09"

/cell_type="marine picoplankton, less than 1.8 um, greater

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/clone_lib="HF200_10-06-02"

/note="Vector: pCC1FOS; North Pacific Subtropical Gyre

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Temperature: 18.53 C Salinity: 35.04 psu Oxygen: 198.8

umol/kg"

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Query Match 50.0%; Score 17; DB 14; Length 955;

Best Local Similarity 82.4%; Pred. No. 47;

Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GAUGAGCCGUCGCGGC 25

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

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AUTHORS Wang,R., Yu,Y., Kim,H.R., Collura,K., Pries,G., Currie,J.,

Soderlund,C. and Hatfield,J.

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http://genome.arizona.edu/stc/sorghum

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85721-0088, USA

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Class: BAC ends.

Location/Qualifiers

1. .1299

/organism="Sorghum propinquum"

/mol_type="genomic DNA"

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/clone="SP_Ba0016N09"

/clone_lib="SP_Ba"

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HindIII; Paterson lab BAC library (HindIII)"

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Qy 3 CAAACUGAUGAGCCGCU 19

||||:||||:||||:
Db 801 CAAACTGATGAGCCGTT 785

RESULT 15 359 bp mRNA linear EST 07-NOV-2005

BW868335

LOCUS BW868335 Amphioxus Branchiostoma floridae unpublished cDNA library,

neurula whole animal Branchiostoma floridae cDNA clone dfne085101

5', mRNA sequence.

ACCESSION BW868335

VERSION BW868335

KEYWORDS EST.

SOURCE Branchiostoma floridae (Florida lancelet)

ORGANISM Branchiostoma floridae

ORIGIN

Query Match 50.0%; Score 17; DB 13; Length 904;

Best Local Similarity 76.5%; Pred. No. 47;

Matches 13; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CAAACUGAUGAGCCGCU 19

||||:||||:||||:
Db 768 CAAACTGATGAGCCGTT 752

RESULT 13 955 bp DNA linear GSS 27-JAN-2006

DUT59063

LOCUS ASNG2280.g2 HF200_10-06-02 uncultured marine microorganism

DEFINITION HF200_10-06-02 genomic clone HF200_082H09, genomic survey

ACCESSION DUT59063

VERSION DUT59063

KEYWORDS GSS.

SOURCE unclutered marine microorganism HF200_10-06-02

ORGANISM unclutered marine microorganism HF200_10-06-02

REFERENCE 1 (bases 1 to 955)

AUTHORS Delong,E.F., Preston,C.M., Mincer,T., Rich,V., Hallam,S.J.,

Frigaard,N.U., Martinez,A., Sullivan,M., Edwards,R., Chisholm,S.W.

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microbial communities in the ocean's interior

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Contact: Susan Lucas, Alex Copeland, Sam Pitluck, Alla Lapidus,

Kerrie Barry, Tjiana Glavinadelrio, David Bruce, Paul Richardson

and Edward Del

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
Branchiostoma.
1 (bases 1 to 359)
Yu, J., Holland, L. Z., Shin-i, T., Kohara, Y., Satou, Y. and Satoh, N.
Expressed genes in Branchiostoma floridae
Unpublished (2005)
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6835
Email: tshini@gene.nig.ac.jp
If you want to have a cDNA clone for this EST or if you have any
questions, please send an e-mail to Nori Satoh
satoh@ascidian.zool.kyoto-u.ac.jp and its cc to Yutaka Satou
(yutaka@ascidian.zool.kyoto-u.ac.jp).

FEATURES
source
Location/Qualifiers

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/clone="bfne085101"
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/dev_stage="neurula"
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cDNA library, neurula whole animal"

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Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 19 UCGCGCGCAACGAAG 34
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DB 45 TCGCGCGCAACGAAG 60

Search completed: August 28, 2006, 10:29:08
Job time : 2336 secs

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REFERENCE 1 (bases 1 to 32)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 101 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned RNA"

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Best Local Similarity 85.2%; Pred. No. 7.7e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUCGCGGGAACG 31
Db 3 AACTGATGAGCCGTTCCGCGGGAACG 29

RESULT 3
AR408005 34 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 98 from patent US 6632057.
ACCESSION AR408005
VERSION AR408005.1 GI:40157992
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 98 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

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Best Local Similarity 85.2%; Pred. No. 7.6e-06;
Matches 23; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUCGCGGGAACG 31
Db 5 AACTGATGAGCCGTTCCGCGGGAACG 31

RESULT 4
AR407999 34 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 92 from patent US 6632057.
ACCESSION AR407999
VERSION AR407999.1 GI:40157986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 92 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES
source Location/Qualifiers
1..34
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN

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Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30

RESULT 5
AR408000 34 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 93 from patent US 6632057.
ACCESSION AR408000
VERSION AR408000.1 GI:40157987
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 93 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 76.5%; Score 26; DB 2; Length 34;
Best Local Similarity 84.6%; Pred. No. 3.4e-05;
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30

RESULT 6
AR408006 34 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 99 from patent US 6632057.
ACCESSION AR408006
VERSION AR408006.1 GI:40157993
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 99 14-OCT-2003;
GFI Aerospace; Paris;
FRX;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 76.5%; Score 26; DB 2; Length 34;
Best Local Similarity 84.6%; Pred. No. 3.4e-05;
Matches 22; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 AACUGAUGAGCCGUCGCGGGAAC 30
Db 5 AACTGATGAGCCGTTCCGCGGGAAC 30

RESULT 7

BD263835 34 bp RNA linear PAT 17-JUL-2003
LOCUS Ageno-associated virus-delivered ribozyme compositions and methods
DEFINITION of use.
ACCESSION BD263835
VERSION BD263835.1 GI:33073603
KEYWORDS JP 2002542805-A/57.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 34)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: JP 2002542805-A 57 17-DEC-2002;
COMMENT UNIVERSITY OF FLORIDA
OS Artificial Sequence
PN JP 2002542805-A/57
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
,CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C12Q1/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC PEPTIDE FH Key
Location/Qualifiers
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 8
AR407997 34 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 90 from patent US 6632057.
DEFINITION AR407997
ACCESSION AR407997
VERSION AR407997.1 GI:40157984
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 90 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
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/mol_type='unassigned RNA'

ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

Db 6 ACTGATGAGCCGTTCCGCGCGGAAC 30
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RESULT 9
AR407998 34 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 91 from patent US 6632057.
DEFINITION AR407998
ACCESSION AR407998
VERSION AR407998.1 GI:40157985
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 91 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
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/mol_type='unassigned RNA'

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Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
||:|||||:|||||
6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 10
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LOCUS Sequence 95 from patent US 6632057.
DEFINITION AR408002
ACCESSION AR408002
VERSION AR408002.1 GI:40157989
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 95 14-OCT-2003;
GPI Aerospace; Paris;
FRX; Location/Qualifiers
1..34
/organism='unknown'
/mol_type='unassigned RNA'

ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
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6 ACTGATGAGCCGTTCCGCGCGGAAC 30

RESULT 11
AR408003 34 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 96 from patent US 6632057.
DEFINITION AR408003
ACCESSION AR408003
VERSION AR408003.1 GI:40157990
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 96 14-OCT-2003;
GPI Aerospace; Paris;
FRX;
FEATURES location/Qualifiers
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Best Local Similarity 84.0%; Pred. No. 0.00015;
Matches 21; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 ACUGAUGAGCCGUCGCGCGGAAC 30
6 ACTGATGAGCCGTCGCGCGGAAC 30
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AR408004
LOCUS AR408004
DEFINITION Sequence 97 from patent US 6632057.
ACCESSION AR408004
VERSION AR408004.1 GI:40157991
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 34)
AUTHORS Fauchet,C.R.J.
TITLE Fixing unit with an end imprint in a threaded terminal portion
JOURNAL Patent: US 6632057-A 97 14-OCT-2003;
GPI Aerospace; Paris;
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source 1..34 /organism="unknown"
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ORIGIN
Query Match 73.5%; Score 25; DB 2; Length 34;
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AX048321
LOCUS AX048321
DEFINITION Sequence 57 from Patent WO0066780.
ACCESSION AX048321
VERSION AX048321.1 GI:11877086
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: WO 006780-A 97 09-NOV-2000;
University of Florida (US)
FEATURES location/Qualifiers

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BD263871
LOCUS BD263871
DEFINITION Adeno-associated virus-delivered ribozyme compositions and methods of use.
ACCESSION BD263871
VERSION BD263871.1 GI:33073639
KEYWORDS JP 2002542805-A/93.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 44)
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: JP 2002542805-A 93 17-DEC-2002;
UNIVERSITY OF FLORIDA
COMMENT OS Artificial Sequence
PN JP 2002542805-A/93
PD 17-DEC-2002
PF 28-APR-2000 JP 2000615402
PR 30-APR-1999 US 60/131942
PI ALFRED S LEWIN,NICHOLAS MUZYCZKA,WILLIAM W HAUSWIRTH PI
CHRISTIAN TESCHENDORF,
PI CORINNA BURGER
PC C12N15/09,A01K67/027,C12N9/00,C12O1/68,C12N15/00 CC
Description of Artificial Sequence: SYNTHETIC OLIGONUCLEOTIDE PH
Key Location/Qualifiers
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AX048357
LOCUS AX048357
DEFINITION Sequence 93 from Patent WO0066780.
ACCESSION AX048357
VERSION AX048357.1 GI:11877122
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Lewin,A.S., Muzyczka,N., Hauswirth,W.W., Teschendorf,C. and Burger,C.
TITLE Adeno-associated virus-delivered ribozyme compositions and methods of use
JOURNAL Patent: WO 006780-A 97 09-NOV-2000;
University of Florida (US)
FEATURES location/Qualifiers

REFERENCE 1
AUTHORS Lewin,A.S., Muzycka,N., Hauewirth,W.W., Teschendorf,C. and
Burger,C.

TITLE Adeno-associated virus-delivered ribozyme compositions and methods
of use

JOURNAL Patent: WO 006780-A 93 09-NOV-2000;
University of Florida (US)

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ORIGIN

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